

LISTING OF CLAIMS

The following listing of claims replaces all prior versions of claims in the application.

Claims 1-13 (canceled)

Claim 14 (currently amended): A method for generating a high-dimensional vector of visualizing sequence data of at least one of a plurality of biopolymer materials represented in a set of sequence data, the method comprising:

for at least one of a plurality of biopolymer materials represented in a set of sequence data, which sequence data lacks ascertainable attributes, comparing sequence data regarding of each biopolymer material to sequence data regarding of each other biopolymer material to provide respective comparison results;

arranging the comparison results in a square matrix indexed by the plurality of biopolymer materials;

creating a high-dimensional context vector for at least one of the biopolymer materials based on a row or column of the square matrix; and

projecting the context vector onto a two- or three-dimensional viewing area; wherein the context vector provides attributes to enable visualization of the sequence data of the respective biopolymer material thereby visualizing sequence data

for at least one of a plurality of biopolymer materials represented in the set of sequence data.

Claim 15 (previously presented): The method according to claim 14, wherein from each row or column of the square matrix, a respective high-dimensional context vector is created for each of the biopolymer materials based on the comparison results in the row or column.

Claim 16 (previously presented): The method according to claim 14, wherein the comparing uses a Basic Local Alignment Search Tool.

Claim 17 (previously presented): The method according to claim 14, wherein the comparing provides comparison results based on an expectation of a relation.

Claim 18 (previously presented): The method according to claim 14, wherein the biopolymer material is protein.

Claim 19 (previously presented): The method according to claim 14, wherein the biopolymer material is nucleic acid.

Claim 20 (currently amended): An apparatus for generating a high-dimensional vector visualizing sequence data for at least one of a plurality of biopolymer materials represented in a set of sequence data, the apparatus comprising:

at least one memory having program instructions,

at least one computer output device for visualizing sequence data, and

at least one processor configured to execute the program instructions to perform the operations of:

~~for at least one of a plurality of biopolymer materials represented in a set of sequence data, which sequence data lacks ascertainable attributes, comparing sequence data regarding of each biopolymer material to sequence data regarding of each other biopolymer material to provide a respective comparison results;~~

arranging the comparison results in a square matrix indexed by the plurality of biopolymer materials;

creating a high-dimensional context vector for at least one of the biopolymer materials based on a row or column of the square matrix; and

projecting the context vector onto a two- or three-dimensional viewing area,
wherein the context vector provides attributes to apparatus enables visualization of the sequence data of the respective biopolymer material.

Claim 21 (currently amended): An apparatus for generating a high-dimensional vector visualizing sequence data for at least one of a plurality of biopolymer materials represented in a set of sequence data, the apparatus comprising:

means for comparing sequence data of each biopolymer material to sequence data of each other biopolymer material to provide respective comparison results;

means for arranging the comparison results in a square matrix indexed by the plurality of biopolymer material;

means for creating a high-dimensional context vector for at least one of the biopolymer materials based on a row or column of the square matrix; and

means for projecting the context vector onto a two- or three-dimensional viewing area,

wherein the ~~context vector provides attributes to apparatus enables~~ visualization of the sequence data of the respective biopolymer material.

Claim 22 (currently amended): A computer-readable medium containing instructions for controlling a computer system to perform a method for ~~generating high-dimensional vector visualizing sequence data for at least one of a plurality of biopolymer materials represented in a set of sequence data, the method comprising:~~

~~for at least one plurality of biopolymer materials represented in a set of sequence data, which sequence data lack ascertainable attributes, comparing sequence data regarding of each biopolymer material to sequence data regarding of each other biopolymer material to provide a respective comparison results;~~

arranging the comparison results in a square matrix indexed by the plurality of biopolymer materials;

creating a high-dimensional context vector for at least one of the biopolymer materials based on a row or column of the square matrix; and
projecting the context vector onto a two- or three-dimensional viewing area,
wherein the context vector provides method enables visualization of the sequence data of the respective biopolymer material.

Claim 23 (previously presented): The method of claim 14, wherein the context vector is utilized for comparison of the biopolymer materials using cluster analysis.

Claim 24 (previously presented): The method of claim 14, wherein the context vector comprises a row or column of an object attribute matrix of comparison results.